

FIG. 1A

1001 GTCAACACTA CTGTTGCCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGGAACAGGTC CTTCTCCAG AACCCCTGCC
 CAGTTGTGAT GACAACGGAA TTCGACGTGG ACGGCTCCGT CGCCGTGGA TGCTCTGCTC ACACCTGTGC ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
 305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlys erGlyAsnLe uGlnAspGlu CysGluGlnL eGluArgSe rPheSerGln AsnProCysLeu
 1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
 AGCACCTCCG GTAACGTGCGA TTCTACGGAA AGGTGTCTGT CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAAGTCAC CACGTCGTGC TCTTGTCTGT
 339 ValGluAl aileAlaAla LysMetArgP heHisArgG l nLeuPheSer GlnAspTrpA laaspSerTh rPheSerVal ValGlnGlnG lnAsnSerAsn
 1201 CCCTGCTCTG AACTGCAGC ECAGGCTACC CATTCCTTCT TTTCTCCATCC TTCCCTTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
 GGGACGAGAC TCTGACGTGC GTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGGAACCTA AGACGACGTC TGGGAGACCA TCGACCCCGAA GGAATCCCCAG
 372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerileL euProLeuL eLeuLeuGln ThrLeuTrp
 1301 CTTTGTCTC TCACACACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA GAAGACGCAG CGTGCTACAC AGCAACCCCG
 GAAACAGGAG AGGTGGTGTG GGCTGACTA AACGTCGGAC ACCACCTCTT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC
 1401 AACCAACCAG GCATTCGCA GCACATCCG TCTGCTCCAG AAGAGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAAAC
 TTGGTTGGTC CGTAAGCGCT CGTGTAGGCG AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTGCGCGATC AAAAGTTTGG
 1501 TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTTCGTATG GTGATTAGCG GCTCACCTCC
 AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAACCGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
 1601 AGCGCTTCTT CCTGTGTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
 TCGCGAAGAA GGACAAAGGG TCCTGGTGGG TCTCCGATTC CTTAGTCACT AAGGGACAAC GGAAGAGGTC CTTCCGTCGG ATTCCCAAGA CTCCACTGAC
 1701 AGAAAAATGT TTCTTTTGTG TGGAAGGCTG GTGCTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
 TCTTTTACAA AAGGAAACAC ACCTTCCGAC CACGAGGTGCG GAGGTGCAGG GAGACTTACC TTCTATTTTT GGACGACCCAC AGAACTGACG AGACGGTCCG
 1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTTGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCCTAGT CCCTTGGGTC ATGATTAAAC
 TTAGGACTTG TAAACCCGTA CTCTCTGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGGTTT AAGGGGATCA GGAACCCAG TACTAATTG
 1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
 TAAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIG. 1B

FIG. 2

hGFra3	1	M	V	R	P	L	N	P	R	P	L	P	P	V	V	L	M	L	L	L	L	L	P	P	S	P	L	P	A	A	G	D	P	L	P	T	E	S	R	L	M	N	S	C	L	Q	A	R	R	K
mGFra3	1	-	-	M	G	L	S	W	S	P	R	P	P	L	L	M	I	L	L	L	V	L	S	L	W	-	L	P	L	G	A	G	N	S	L	A	T	E	N	R	F	V	N	S	C	T	Q	A	R	K

hGFra3	51	C	Q	A	D	P	T	C	S	A	A	Y	H	L	D	S	C	T	S	S	I	S	T	P	L	P	S	E	E	P	S	V	P	A	D	C	L	E	A	A	Q	L	R	N	S	S	L	I	G		
mGFra3	48	C	E	A	N	P	A	C	K	A	A	Y	Q	H	L	G	S	C	T	S	S	L	S	R	P	L	P	L	E	E	S	A	M	S	A	D	C	L	E	A	A	E	Q	L	R	N	S	S	L	I	D

hGFra3	101	C	M	C	H	R	R	M	K	N	Q	V	A	C	L	D	I	Y	W	T	V	H	R	A	R	S	L	G	N	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
mGFra3	98	C	R	C	H	R	R	M	K	H	Q	A	T	C	L	D	I	Y	W	T	V	H	P	A	R	S	L	G	D	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S

hGFra3	151	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	N	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	P	H	C	Q	R	H	V	C	L	R	Q	L
mGFra3	148	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	H	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	I	R	C	Q	R	H	L	C	L	A	Q	L

hGFra3	201	L	T	F	F	E	K	A	A	E	P	H	A	Q	G	L	L	C	P	C	A	P	N	D	R	G	C	G	E	R	R	R	N	T	I	A	P	N	C	A	L	P	P	V	A	P	N	C	L	E
mGFra3	198	R	S	F	F	E	K	A	A	E	S	H	A	Q	G	L	L	C	P	C	A	P	E	D	A	G	C	G	E	R	R	R	N	T	I	A	P	S	C	A	L	P	S	V	T	P	N	C	L	D

hGFra3	251	L	R	R	L	C	F	S	D	P	L	C	R	S	R	L	V	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M
mGFra3	248	L	R	S	F	C	R	A	D	P	L	C	R	S	R	L	M	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M

hGFra3	301	T	P	N	F	V	S	N	V	N	T	S	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	E	C	E	M	L	E	G	F	F	S	H	N	P	C	L	T	E	A	I	A	A	K	M	R
mGFra3	298	T	P	N	F	I	S	K	V	N	T	T	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	C	E	Q	L	E	R	S	F	S	Q	N	P	C	L	V	E	A	I	A	A	K	M	R	

hGFra3	351	F	H	S	Q	L	F	S	Q	D	W	P	H	P	T	F	A	V	M	A	H	Q	N	E	N	P	A	V	R	P	Q	P	W	V	P	S	L	F	S	C	T	L	P	L	I	L	L	S	L	W
mGFra3	348	F	H	R	Q	L	F	S	Q	D	W	A	D	S	T	F	S	V	V	Q	Q	N	S	N	P	A	L	R	L	Q	P	R	L	P	I	L	S	F	S	I	L	P	L	I	L	Q	T	L	W	

FIG. 3

48613 1 MVRPLNPRPLPPVVLMLLLLLPPSPPLAAGDPLPTESRLMNSCLQARRK
48614 1 MVRPLNPRPLPPVVLMLLLLLPPSPPLAAGDPLPTESRLMNSCLQARRK

48613 51 CQADPTCSAAYHHLDSDCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614 51 CQADPTCSAAYHHLDSDCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRRMKNQVACLDIYWTVHRRARSL GNYELDVSPYEDTVTSKPWKMNLS
48614 101 CMCHRRRMKNQVACLDIYWTVHRRARSL

48613 151 KLNMLKPP DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614 127 DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613 201 LTFEKEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614 170 LTFEKEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTATEQSRCLRAYLGLIGTAM
48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLLSLW
48614 320 FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLLSLW

DNA48613.orf	1	A	T	G	G	T	G	C	G	C	C	C	C	C	T	G	A	A	C	C	C	G	A	C	C	G	C	T	G	C	C	G	C	C	T	G	A	T	G	T	T																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
GENFRa1.orf	1

FIG. 5A

DNA48613.orf	398	TCTCCCCCTATGAAG.....ACACAGTGA	CCAGC
GENFRa1.orf	356	CCCATATGAACCAAGTTA.....ACAGC	CAGATTGTCA
GENFRa2.orf	374	CCTCCCCCTATGAAGCCGGTGACCTCCCGCCTCTCGGACATCT	CAAGGCTT
DNA48613.orf	427	AACCCCTGGAAATGAATCTCAGCAAACTGAACAATGCTCAAA	CCAGACTC
GENFRa1.orf	388	GATATATTCCGGGTGGTCCCAATTCATATCAGTGGAGCA	CAATCCCAAAGG
GENFRa2.orf	424	GCTTCAATCTTCTCAGGGAACAAGGGCAAGACCCGGTGT	CAAGCCAAAGAG
DNA48613.orf	477	AGACCTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGACAA	GTGTG
GENFRa1.orf	438	GACCACTGCCTGGATGCAAGCGAAGGCCCTGCAACCTCGAC	GACATTTGCA
GENFRa2.orf	474	CAACCAATTGCCCTGGATGCTGCCAAGGCCCTGCAACCTGAAT	GACAACTGCA
DNA48613.orf	527	ACCGGCTGCGGCAAGGCCCTACGGGGAGGCGTGCTCCGG	GCGCCCACTG...C
GENFRa1.orf	488	AGAAGTACAAGTTCGGCGGTACATCAACCCCGTGCACCA	CACAGCTGTCTC...C
GENFRa2.orf	524	AGAGCTGCGGCTCTCCTACATCTCCATCTTGCAACCGCGA	GATCTCGCC
DNA48613.orf	574	CAGCGCCACGCTCTGCTTCAAGGCAAGCTGCTC	ACTTTCTTCGAGAGGCGCGC
GENFRa1.orf	535	AATGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGG	CAGTTCTT
GENFRa2.orf	574	ACCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCT	GCGCCAGTTCTT
DNA48613.orf	624	CGAG.....CCCAACGCGCAGGCGCTGCTACTGTG	CCCATGTGCCCCCA
GENFRa1.orf	585	TGACAAAGGTCCCGGCCAAGCAACAGCTACGGAAATGCTCTTCT	GCTCCTGCC
GENFRa2.orf	624	CGACCGGGTGCCCAAGCGAGTACACCTACCGCAATGCTCTTCT	GCTCCTGCC
DNA48613.orf	668	ACGACCGGGGCTGCGGGGAGCGCCGGCGCAAC	CCATCGCCCAACTGC
GENFRa1.orf	635	GGGACATCGCCTGCAACAGAGCGGAGGCGGACAG	ACCATCGTGCTGTGC
GENFRa2.orf	674	AGACCAAGGCGTGCGCTGAGCGCCGCGCGGCA	ACCATCTGCCCAGCTGC

FIG. 5B

DNA48613.orf	718	G	C	G	C	T	G	C	C	...	G	C	C	T	G	T	G	C	C	C	C	C	A	A	C	T	G	C	C	T	G	G	A	G	C	T	G	C	G	G	C	G	C	T	C	T	G			
GENFRa1.orf	685	T	C	C	T	A	T	G	A	G	A	G	A	G	A	G	C	C	C	A	A	C	T	G	T	T	G	A	A	T	T	G	C	A	G	A	C	T	C	C	T	G	C	T	G					
GENFRa2.orf	724	T	C	C	T	A	T	G	A	G	A	G	A	G	A	G	C	C	C	A	A	C	T	G	C	C	T	G	G	A	C	C	T	G	G	A	C	T	G	C	G	T	G	G	C	G	T	G		
DNA48613.orf	765	C	T	T	C	T	C	G	A	C	C	C	G	C	T	T	T	G	C	A	G	A	T	C	A	C	G	C	C	T	G	G	A	T	T	T	C	C	A	G	A	C	C	C	A	C	T			
GENFRa1.orf	735	C	A	A	G	A	C	G	A	A	T	T	A	C	A	T	C	T	G	C	A	G	A	T	C	T	C	G	C	C	T	T	G	C	G	G	A	T	T	T	T	T	T	A	C	C	A	A	C	T
GENFRa2.orf	774	C	C	G	A	C	T	G	A	C	C	A	C	C	T	G	T	C	G	G	T	C	C	G	G	C	T	G	G	C	C	T	G	G	C	C	A	T	T	C	C	A	T	T	G	C	C	A	A	T
DNA48613.orf	815	G	C	C	A	T	C	C	C	A	T	G	G	A	C	T	T	G	T	G	C	A	A	C	A	G	A	G	C	A	G	T	C	C	A	G	A	...												
GENFRa1.orf	785	G	C	C	A	G	C	C	A	G	A	T	C	A	G	T	C	T	G	T	C	A	G	C	A	G	T	C	T	A	A	A	G	A	A	A	C	T	A	C	G	C	T							
GENFRa2.orf	824	G	T	C	G	A	G	C	C	T	C	C	T	A	C	C	A	G	A	C	G	G	T	C	A	C	C	A	G	C	T	G	C	C	T	G	C	G	A	C	A	A	T	T	A	C	C	A	G	
DNA48613.orf	862	...	T	G	T	C	T	A	C	G	A	G	C	A	T	A	C	T	G	G	G	G	C	T	G	A	T	T	G	G	A	C	T	G	C	A	T	G	A	C	C	C	C	C	C	A	A			
GENFRa1.orf	835	G	A	C	T	G	C	T	C	C	T	C	G	C	C	T	A	C	T	C	G	G	G	C	T	A	T	T	G	C	A	C	A	G	T	C	A	T	G	A	C	C	C	C	C	C	A	A		
GENFRa2.orf	874	G	C	G	T	G	T	C	T	G	G	G	C	T	C	T	T	A	T	G	C	T	G	G	C	A	T	G	A	T	T	G	G	T	T	T	G	A	C	A	T	G	A	C	A	C	C	T	A	A
DNA48613.orf	909	C	T	T	T	G	T	C	A	G	C	A	A	T	G	T	C	A	...	A	C	A	C	C	A	G	T	G	C	C	T	T	A	A	G	C	T	G	C	A	C	T								
GENFRa1.orf	885	C	T	A	C	A	T	A	G	A	C	T	C	C	A	G	T	A	...	G	C	C	T	C	A	G	T	G	T	G	G	C	C	C	C	C	A	T	G	G	T	G	T	G	A	C	T			
GENFRa2.orf	924	C	T	A	T	G	T	G	A	C	T	C	C	A	G	C	C	C	C	A	C	T	G	G	C	A	T	C	G	T	G	T	G	T	C	C	C	C	T	G	G	T	G	C	A	G	C	T		
DNA48613.orf	953	G	C	C	G	A	G	C	A	G	T	G	G	C	A	A	C	T	T	G	C	A	G	G	A	G	G	A	G	T	G	A	A	A	T	G	C	T	G	G	A	A	G	G	T	T	C			
GENFRa1.orf	929	G	C	A	G	C	A	C	A	G	T	G	G	G	A	A	C	G	A	C	C	T	A	G	A	G	A	G	T	G	C	T	T	G	A	A	A	T	T	C	T	T	G	A	A	T	T	C		
GENFRa2.orf	974	G	T	C	G	T	G	G	C	A	G	C	G	G	G	A	A	C	A	T	G	G	A	G	G	A	G	T	G	T	G	A	A	G	T	T	C	C	T	C	A	G	G	G	A	C	G			
DNA48613.orf	1003	T	T	C	T	C	C	C	A	C	A	A	C	C	C	C	T	T	G	C	C	T	C	A	C	G	G	A	T	T	G	C	A	T	T	A	A	G	C	T	A	A	G	A	T	T	T			
GENFRa1.orf	979	T	T	C	A	A	G	A	C	A	A	T	A	C	A	T	G	T	C	T	T	A	A	A	A	A	T	G	C	A	T	T	C	A	A	G	C	C	T	T	T	G	G	C	A	A	T	G	G	
GENFRa2.orf	1024	T	T	C	A	C	C	G	A	G	A	A	C	C	C	A	T	G	C	C	T	C	G	G	A	A	C	G	C	C	A	T	C	C	A	G	C	C	A	T	T	T	G	G	C	A	A	C	G	G

FIG. 5C

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
 GENFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C C T T C C C A G T A C A G A C C A C C A C T G
 GENFRa2.orf 1074 C A C G G A C G T G A A C G T G T C C C C A A A G G C C C C T C G T T C A G G C C A C C C A G G

 DNA48613.orf 1103 T G G C C A C A C C A G A A T G A A A A C C C T G C T G T A G G G C C A C A G C C C T G G G T G C C C
 GENFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C C G G G T T A A G A A C A A C C C C T G G G C C A G C A
 GENFRa2.orf 1124 C C C C T C G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

 DNA48613.orf 1153 T C T C T T T T C C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
 GENFRa1.orf 1129 G G G T C T G A G A A T G A A A T T C C C A C T C A T G T T T G C C A C C G T G T G C A A A T T T
 GENFRa2.orf 1174 A C C A G C T T G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

 DNA48613.orf 1203 G
 GENFRa1.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T G T C G G G C A A T A C A C A C C T C T G T A
 GENFRa2.orf 1224 G G G G C T G A A G G C C A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

 GENFRa1.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G G T G C T T C C A G C C A C A T A
 GENFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

 GENFRa1.orf 1279 A C C A C A A A T C A A T G G C T G C T C C T C C A A G C T G T G G T C T G A G C C C A C T G C T
 GENFRa2.orf 1324 G G C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G T C C T

 GENFRa1.orf 1329 G G T C C T G G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T A C A G A A A C A T
 GENFRa2.orf 1374 G A T G C T G A A A C A G G C C T T G T A G

 GENFRa1.orf 1379 C A T A G

FIG. 5D

REPLACEMENT SHEET

DNA48613
GDNFRa1
GDNFRa2

1 M V R P L N P R P L P P V V L M L L L P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
1 M F L A T - - - L Y F A L - - P L L D L L L S A - - E V S G G D - - - - R L - - D C V K A S D Q
1 M I L A N V F C L F F F L D E T L R S L A S P S - - S L Q G P E L H G W R P P V - - D C V R A N E L

DNA48613
GDNFRa1
GDNFRa2

51 G Q A D P T C S A A Y H H L D S C T S S I S T P L P - S E E P S V P A D G L E A A Q Q L R N S S L I
36 C L K E Q S C S T K Y R T L R Q C V A G K E T N F S L A S G L E A K D E C R S A M E A L K Q K S L Y
47 C A A E S N C S S R Y R T L R Q C L A G R D R N - - - - T M L A N K E C Q A A L E V L Q E S P L Y

DNA48613
GDNFRa1
GDNFRa2

100 G C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L
86 N C R C K R G M K K E K N C L R I Y W S M Y Q S L - Q G N D L L E D S P Y E P V N S R L S D I F R V
92 D C R C K R G M K K E L Q C L Q I Y W S I H L G L T E G E E F Y E A S P Y E P V T S R L S D I F R L

DNA48613
GDNFRa1
GDNFRa2

150 S K L - - - - - N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S - - - -
135 V P F I S - - - V E H I - - P K G N N C L D A A K A C N L D D I C K K Y R S A Y I T P C T T S V S -
142 A S I F S G T G A D P V V S A K S N H C L D A A K A C N L N D N C K K L R S S Y I S I C N R E I S P

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GDNFRa1
GDNFRa2

188 G P H C Q R H V C L R Q L L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P
179 N D V C N R R K C H K A L R Q F F D K V P A K H S Y G M L F C S C - - R O I A C T E R R R Q T I V P
192 T E R C N R R K C H K A L R Q F F D R V P S E Y T Y R M L F C S C - - Q D Q A C A E R R R Q T I L P

DNA48613
GDNFRa1
GDNFRa2

238 N C A L P P V A - P N G L E L R R L C F S D P L C R S R L V D F Q T H C H P - M D I L G T C A T E Q
227 V C S Y E E R E K P N C L N L Q D S C K T N Y I C R S R L A D F F T N C Q P E S R S V S S C L K E N
240 S C S Y E D K E K P N C L D L R G V C R T D H L C R S R L A D F H A N C R A S Y Q T V T S C P A D N

DNA48613
GDNFRa1
GDNFRa2

286 - S R C L R A Y L G L I G T A M T P N F V S N V - - N T S V A L S C T C R G S G N L Q E E C E M L E
277 Y A D C L L A Y S G L I G T V M T P N Y I D S S - - S L S V A P W C D C S N S G N D L E E C L K F L
290 Y Q A C L G S Y A G M I G F D M T P N Y V D S S P T G I V V S P W C S C R G S G N M E E E C E K F L

DNA48613
GDNFRa1
GDNFRa2

333 G F F S H N P C L T E A I A A - - - - - - - - - - - - - - - - K M R F H S Q L F S
325 N F F K D N T C L K N A I Q A F G N G S D V T V W Q P A F P V Q T T T A T T T T A L R V K N K P L G
340 R D F T E N P C L R N A I Q A F G N G T D V N V S P K G P S F Q A T Q A P R V E K T P S L P D D L S

DNA48613
GDNFRa1
GDNFRa2

358 Q - - - - - D W P H P T F A V M A H Q N E N P A V R P Q - - - - - - - - - - - - - - -
375 P A G S E N E I P T H V L P P C A N L Q A Q K L K S N V S G N T H L C I S N G N Y E K E G L G A S S
390 D S T S - - L G T S V I T T C T S V Q E Q G L K A N N S K E L S M C F T - - E L T T N I I P G S N

DNA48613
GDNFRa1
GDNFRa2

381 - - - - P W V P S L F S C T L P L I L L S L W - - - - - - - - - - - - - - -
425 H I T T K S M A A P P S C G L S P L L V L V V T A L S T L L S L T E T S
435 K V I K P N S G P S R A R P S A A L T V L S V L M L K Q A L - - - - -

FIG. 6

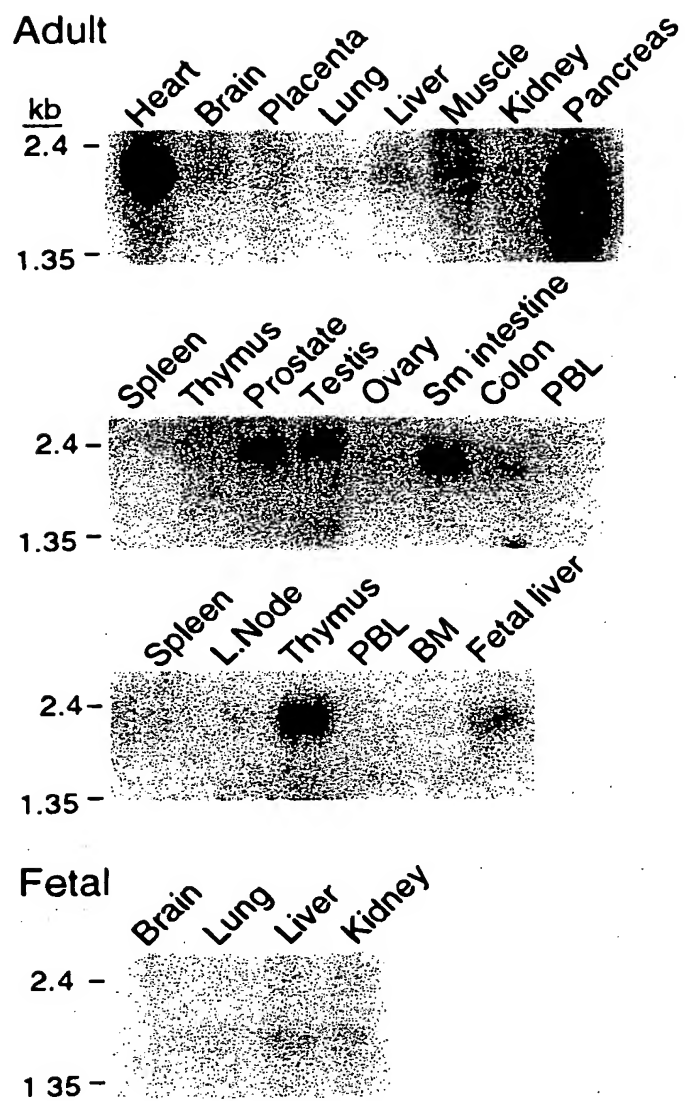


FIG. 7

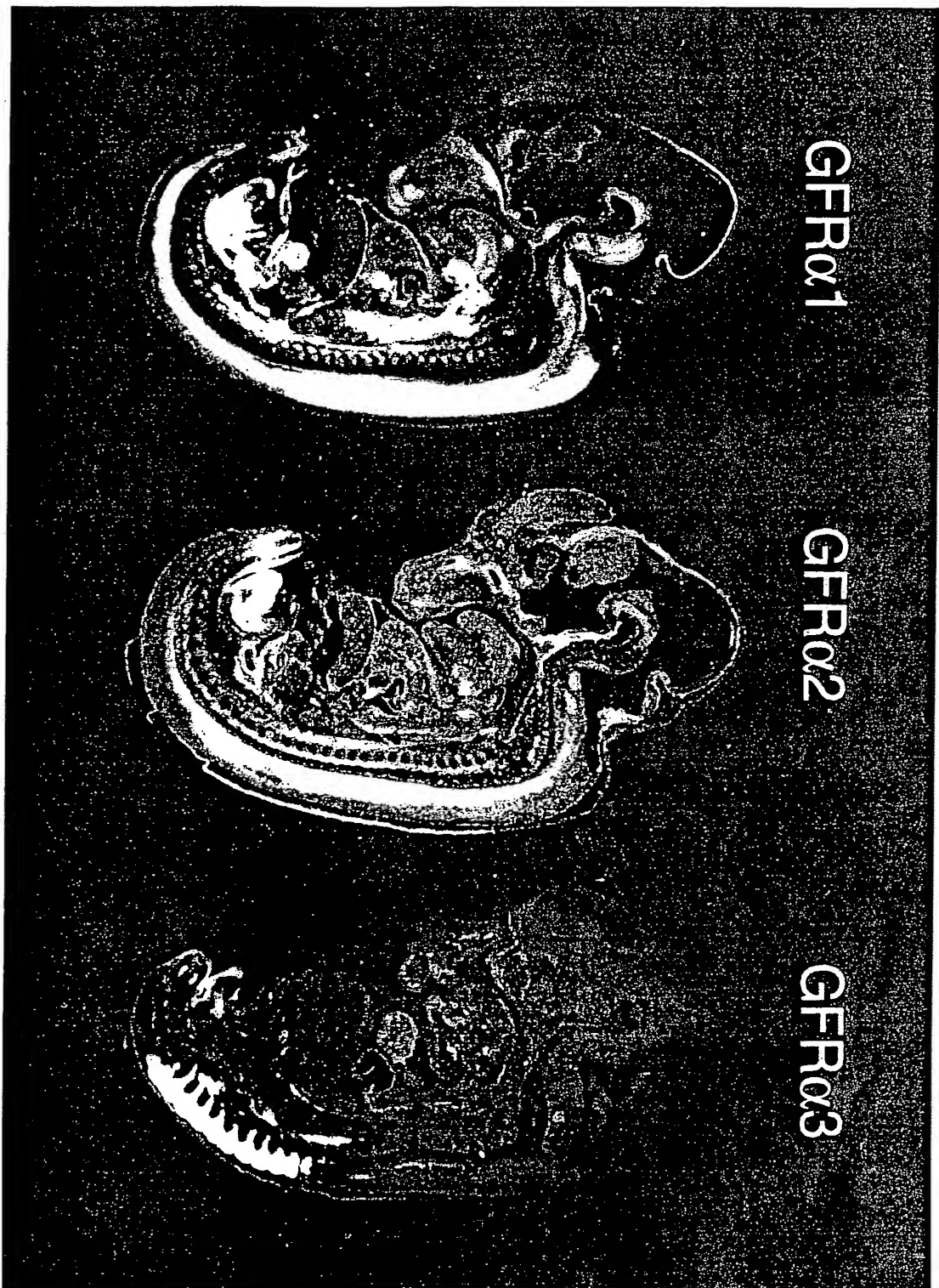
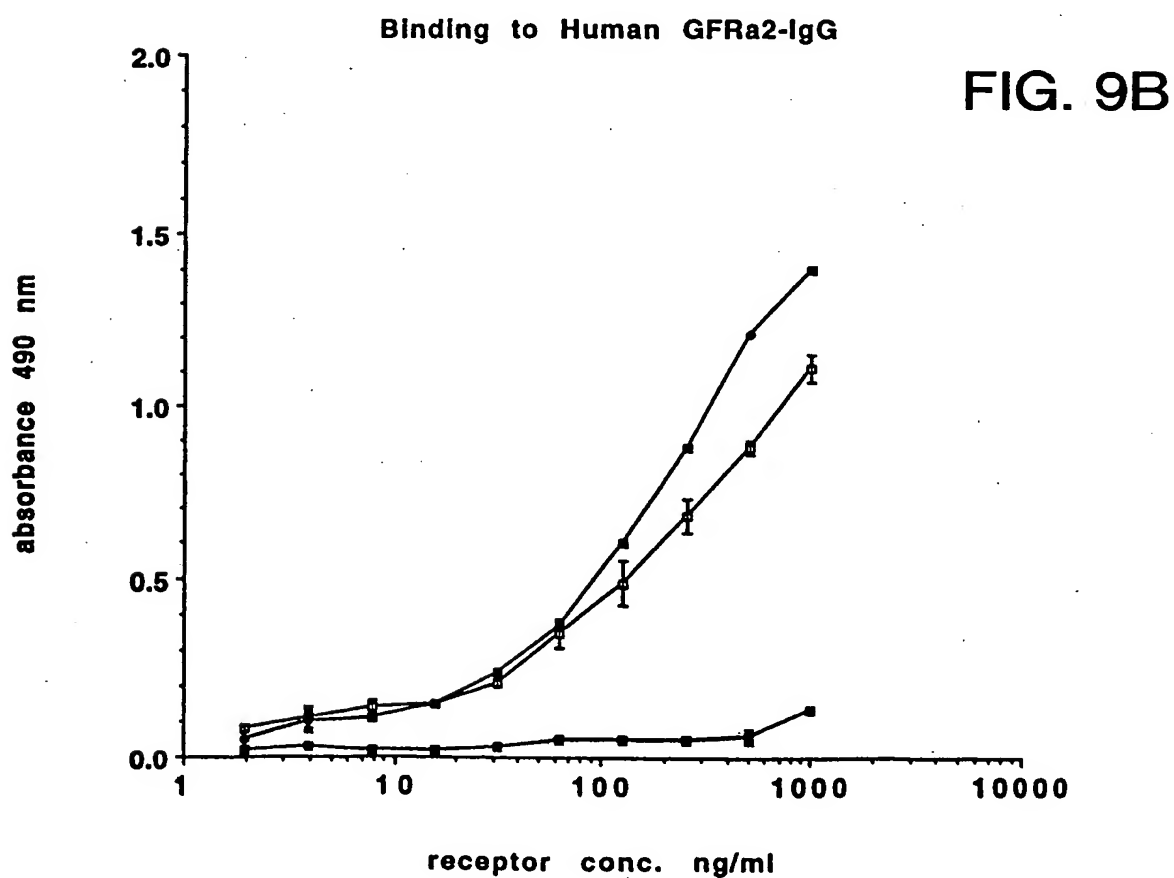
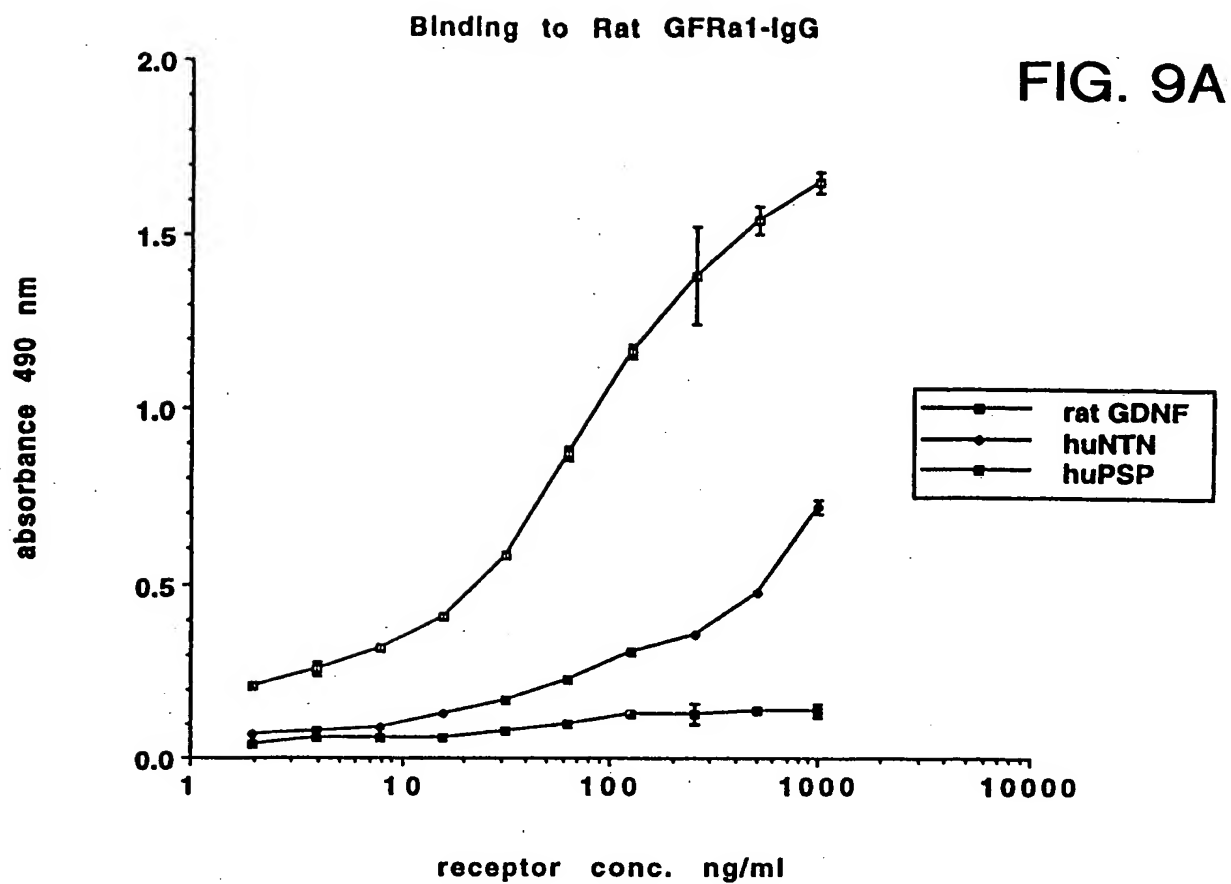
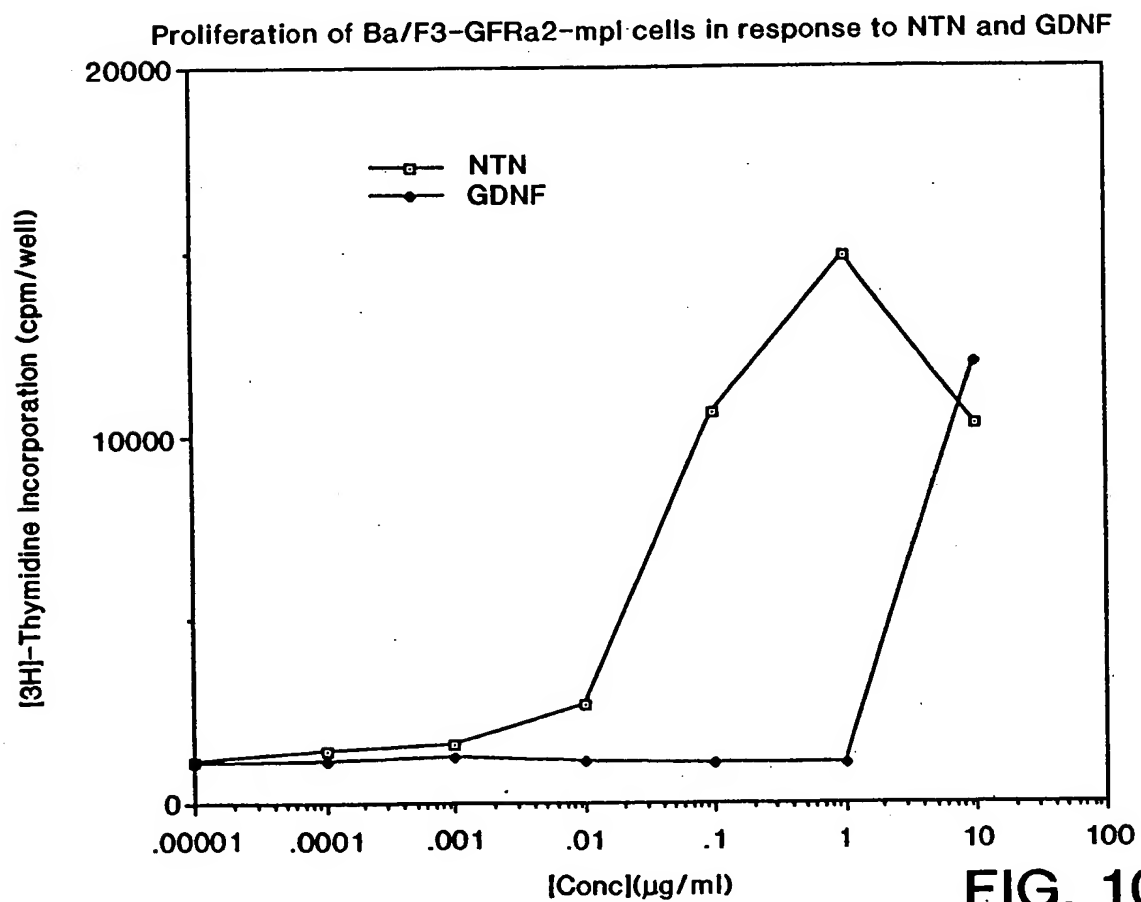
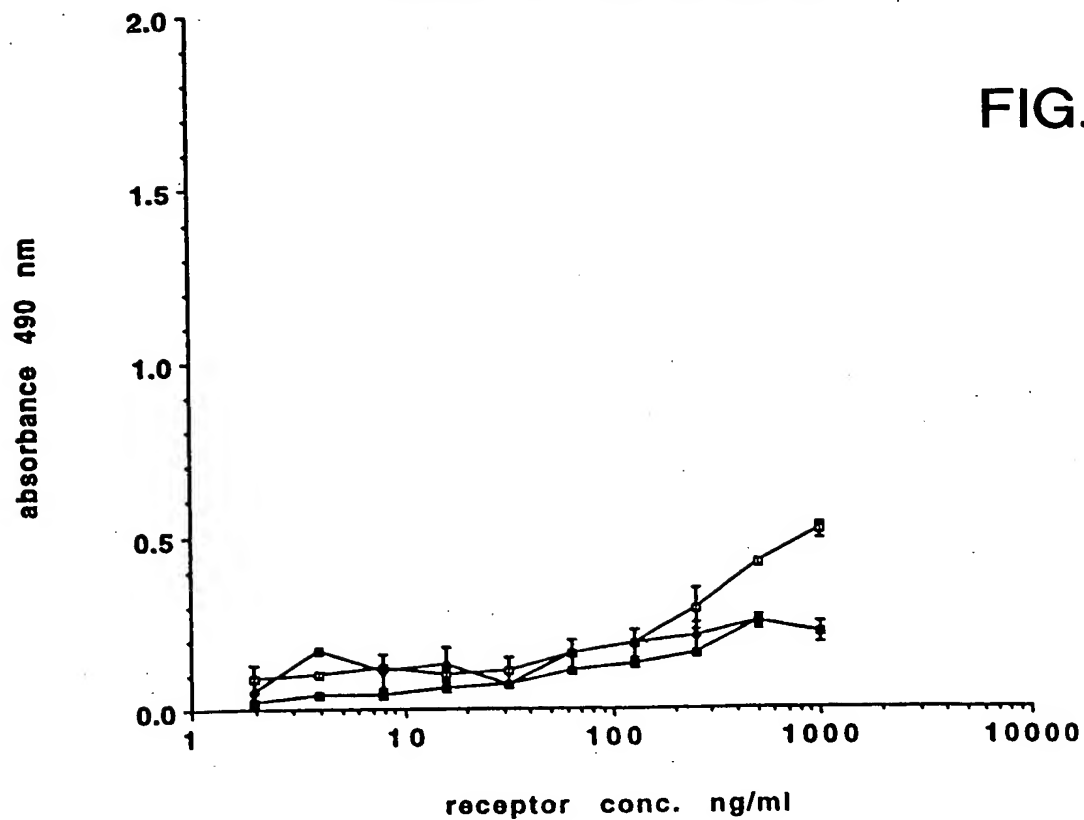


FIG. 8



Binding to Human GFRa3-IgG



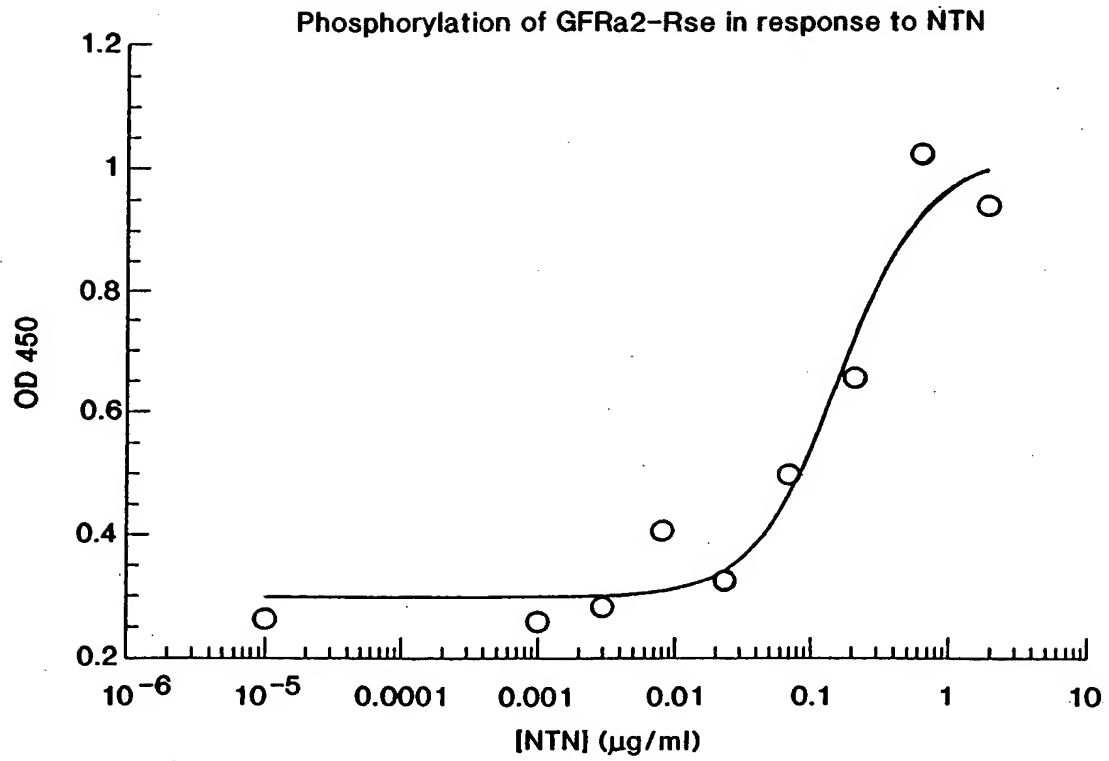


FIG. 11

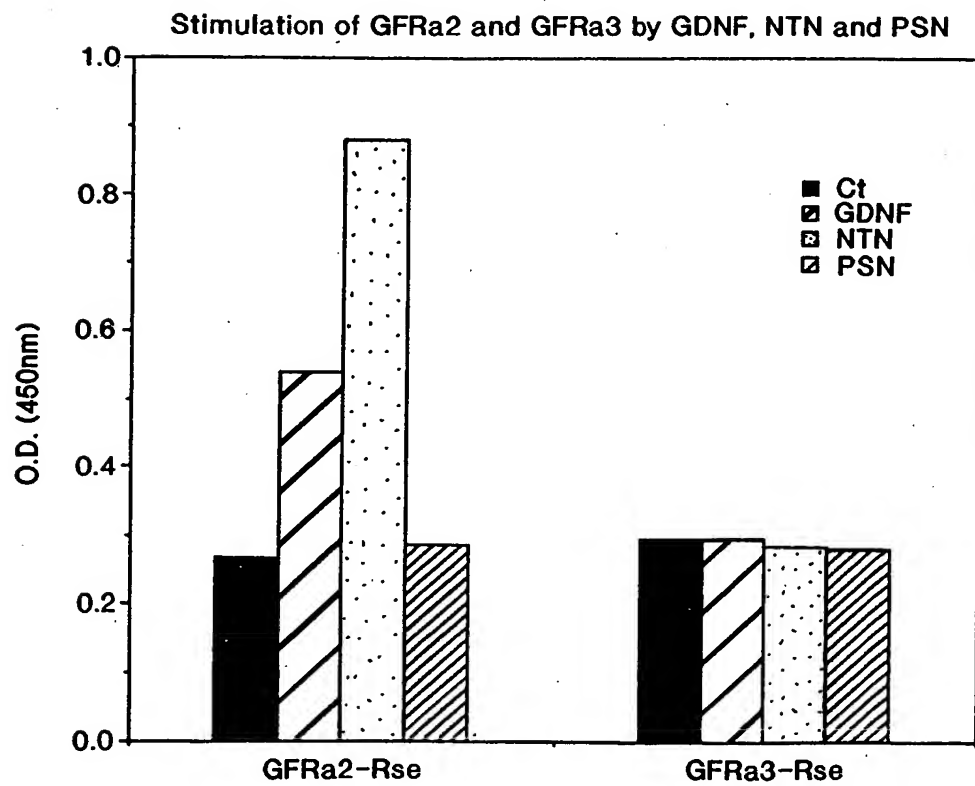


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

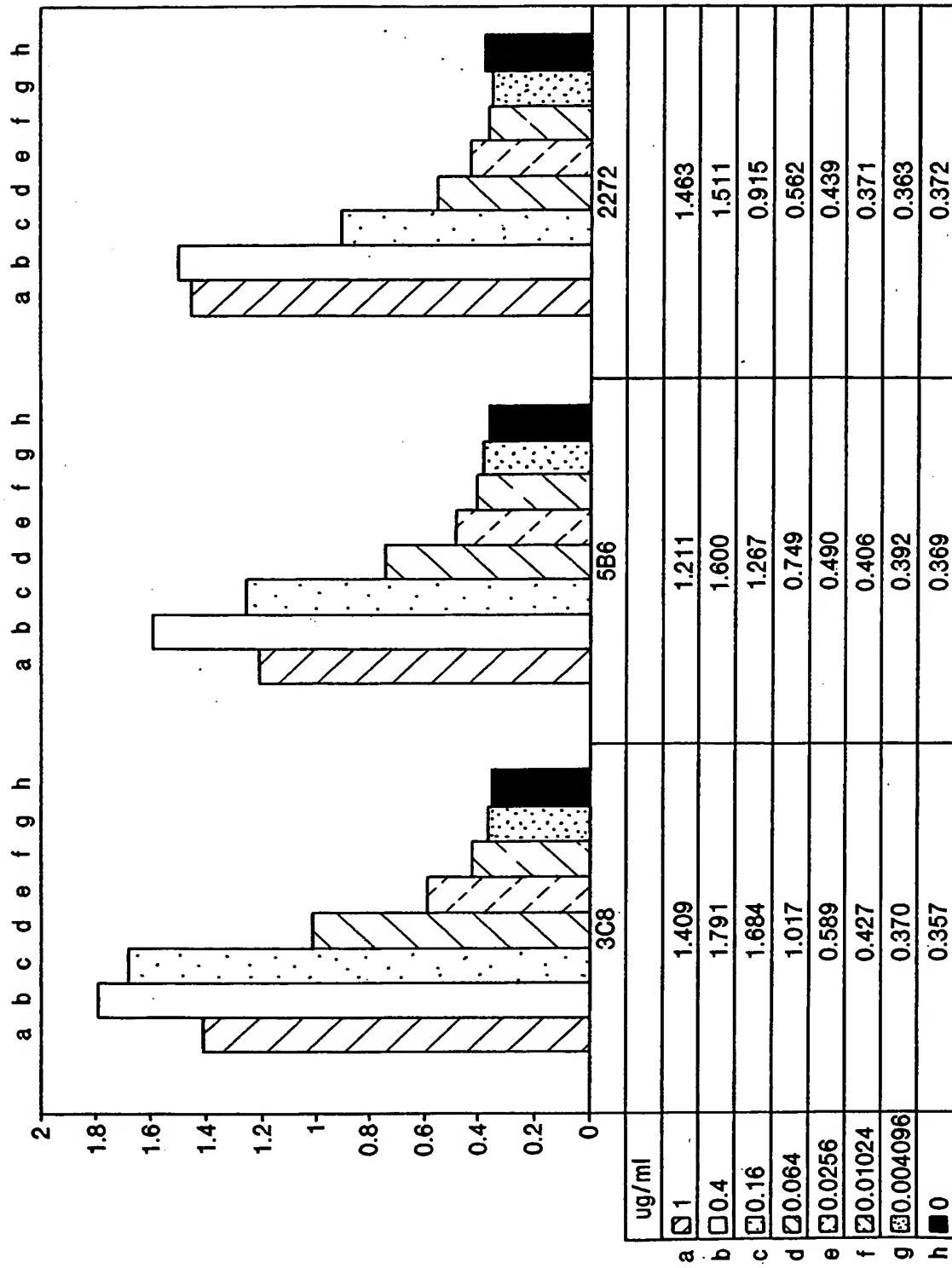


FIG. 13

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